



SUBSTITUTE SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: PULST, STEFAN M.
- (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR ATAXIA-2 AND PRODUCTS RELATED THERETO
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
(B) STREET: 119 NORTH FOURTH STREET, SUITE 203
(C) CITY: MINNEAPOLIS
(D) STATE: MINNESOTA
(E) COUNTRY: 55401
(F) ZIP: 55401
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/981,998
(B) FILING DATE: 11-MAY-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO 97/42314
(B) FILING DATE: 08-MAY-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/727,084
(B) FILING DATE: 08-OCT-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/022,207
(B) FILING DATE: 19-JUL-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/017,388
(B) FILING DATE: 08-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: MUETING, ANN M.
(B) REGISTRATION NUMBER: 33,977
(C) REFERENCE/DOCKET NUMBER: 232.00010120
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 612-305-1217
(B) TELEFAX: 612-305-1228

(2) INFORMATION FOR SEQ ID NO:1:

- a1*
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGTAGCAA CGGAAACGGC GGCGCGCGT TTGGCCCGG CTCCGGCGG CTCCTGGTC	60
TCGGCGGGCC TCCCCGCCCTT TCCTCGTCG TCCTCTCCC CCTCGCCAGC CCGGGCGCCC	120
CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TGCGTCCCCG CCGCGTTCCG	180
GCGTCTCCTT GGCGCGCCCG GCTCCCGGCT GTCCCCGCCG GGCGTGCGAG CCGGTGTATG	240
GGCCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC	300
AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA	360
AGCCCGGCAG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTCGCCG TCCTCGTCCT	420
CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGCG	480
GGAGGCCCCGG CCTGGGCAGG TGGGTGTGG CACCCC	516

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 163..4101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG	60
GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG	120
CACCTCCGCT CCCACCCGGC GCCTCGGCAGC GCCCGCCCTC CG ATG CGC TCA GCG	174
Met Arg Ser Ala	

q1

cont

GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe	222
5 10 15 20	
GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg	270
25 30 35	
CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC Arg Ser Gly Arg Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser	318
40 45 50	
GCC GCC CCT CCC CCG CCC GGC CCC CCC CCT CCC TCC CGG CAG AGC Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Ser Arg Gln Ser	366
55 60 65	
TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly	414
70 75 80	
GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro	462
85 90 95 100	
CCC CGC CCC TTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala	510
105 110 115	
CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser	558
120 125 130	
CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro	606
135 140 145	
CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys	654
150 155 160	
CCC CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG Pro Gln	702
165 170 175 180	
CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg	750
185 190 195	
AAG CCC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser	798
200 205 210	
CCG TCC TCG TCC TCG GTC TCC TCG TCG GCC ACG GCT CCC TCC TCG Pro Ser Ser Ser Val Ser Ser Ser Ala Thr Ala Pro Ser Ser	846
215 220 225	

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cont

GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly 230 235 240	894
CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly 245 250 255 260	942
ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly 265 270 275	990
TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val 280 285 290	1038
TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His 295 300 305	1086
GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG Glu Lys Ser Thr Glu Ser Ser Gly Pro Lys Arg Glu Glu Ile Met 310 315 320	1134
GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys 325 330 335 340	1182
GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala 345 350 355	1230
ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro 360 365 370	1278
TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu 375 380 385	1326
AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn 390 395 400	1374
GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser 405 410 415 420	1422
TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg 425 430 435	1470
GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln 440 445 450	1518

*A1
Cont*

TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA	1566
Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu	
455 460 465	
AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC	1614
Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser	
470 475 480	
ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA	1662
Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg	
485 490 495 500	
GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC	1710
Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly	
505 510 515	
CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA	1758
Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser	
520 525 530	
GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT	1806
Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly	
535 540 545	
GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT	1854
Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro Pro Ser	
550 555 560	
CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CCT	1902
Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr Pro	
565 570 575 580	
ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC CCG TCT	1950
Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser	
585 590 595	
CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA	1998
His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys	
600 605 610	
CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC CAG CGA	2046
Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg	
615 620 625	
CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA TCC AGT	2094
His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile Ser Ser	
630 635 640	
GGC CTA GAA TTT GTA TCC CAC AAC CCA CCC AGT GAA GCA GCT ACT CCT	2142
Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Thr Pro	
645 650 655 660	
CCA GTA GCA AGG ACC AGT CCC TCG GGG GGA ACG TGG TCA TCA GTG GTC	2190
Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp Ser Ser Val Val	
665 670 675	

AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG TCT CCC Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro 680 685 690	2238
AGA CAG AAC AGT ATT GGA AAT ACC CCC AGT GGG CCA GTT CTT GCT TCT Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro Val Leu Ala Ser 695 700 705	2286
CCC CAA GCT GGT ATT ATT CCA ACT GAA GCT GTT GCC ATG CCT ATT CCA Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala Met Pro Ile Pro 710 715 720	2334
GCT GCA TCT CCT ACG CCT GCT AGT CCT GCA TCG AAC AGA GCT GTT ACC Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Val Thr 725 730 735 740	2382
CCT TCT AGT GAG GCT AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn 745 750 755	2430
TCT CCT GCA GGG AAT AAA GAA AAT ATT AAA CCC AAT GAA ACA TCA CCT Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn Glu Thr Ser Pro 760 765 770	2478
AGC TTC TCA AAA GCT GAA AAC AAA GGT ATA TCA CCA GTT GTT TCT GAA Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro Val Val Ser Glu 775 780 785	2526
CAT AGA AAA CAG ATT GAT GAT TTA AAG AAA TTT AAG AAT GAT TTT AGG His Arg Lys Gln Ile Asp Asp Leu Lys Phe Lys Asn Asp Phe Arg 790 795 800	2574
TTA CAG CCA AGT TCT ACT TCT GAA TCT ATG GAT CAA CTA CTA AAC AAA Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Asn Lys 805 810 815 820	2622
AAT AGA GAG GGA GAA AAA TCA AGA GAT TTG ATC AAA GAC AAA ATT GAA Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Ile Glu 825 830 835	2670
CCA AGT GCT AAG GAT TCT TTC ATT GAA AAT AGC AGC AGC AAC TGT ACC Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser Asn Cys Thr 840 845 850	2718
AGT GGC AGC AGC AAG CCG AAT AGC CCC AGC ATT TCC CCT TCA ATA CTT Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser Pro Ser Ile Leu 855 860 865	2766
AGT AAC ACG GAG CAC AAG AGG GGA CCT GAG GTC ACT TCC CAA GGG GTT Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val 870 875 880	2814
CAG ACT TCC AGC CCA GCA TGT AAA CAA GAG AAA GAC GAT AAG GAA GAG Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Lys Glu Glu 885 890 895 900	2862

AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT CCC AAT Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn 905 910 915	2910
GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT TCT ACT Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr 920 925 930	2958
ACC CCA ACT TCA CCT CGG CCT CAA GCA CAA CCT AGC CCA TCT ATG GTG Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val 935 940 945	3006
GGT CAT CAA CAG CCA ACT CCA GTT TAT ACT CAG CCT GTT TGT TTT GCA Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro Val Cys Phe Ala 950 955 960	3054
CCA AAT ATG ATG TAT CCA GTC CCA GTG AGC CCA GGC GTG CAA CCT TTA Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu 965 970 975 980	3102
TAC CCA ATA CCT ATG ACG CCC ATG CCA GTG AAT CAA GCC AAG ACA TAT Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr 985 990 995	3150
AGA GCA GTA CCA AAT ATG CCC CAA CAG CGG CAA GAC CAG CAT CAT CAG Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His His Gln 1000 1005 1010	3198
AGT GCC ATG ATG CAC CCA GCG TCA GCA GCG GGC CCA CCG ATT GCA GCC Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile Ala Ala 1015 1020 1025	3246
ACC CCA CCA GCT TAC TCC ACG CAA TAT GTT GCC TAC AGT CCT CAG CAG Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro Gln Gln 1030 1035 1040	3294
TTC CCA AAT CAG CCC CTT GTT CAG CAT GTG CCA CAT TAT CAG TCT CAG Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln Ser Gln 1045 1050 1055 1060	3342
CAT CCT CAT GTC TAT AGT CCT GTA ATA CAG GGT AAT GCT AGA ATG ATG His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg Met Met 1065 1070 1075	3390
GCA CCA CCA ACA CAC GCC CAG CCT GGT TTA GTA TCT TCT TCA GCA ACT Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser Ser Ala Thr 1080 1085 1090	3438
CAG TAC GGG GCT CAT GAG CAG ACG CAT GCG ATG TAT GCA TGT CCC AAA Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys Pro Lys 1095 1100 1105	3486
TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC ATT TCC Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala Ile Ser 1110 1115 1120	3534

ACG GGC TCC CTT GCT CAG CAG TAT GCG CAC CCT AAC GCT ACC CTG CAC Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Thr Leu His 1125 1130 1135 1140	3582
CCA CAT ACT CCA CAC CCT CAG CCT TCA GCT ACC CCC ACT GGA CAG CAG Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly Gln Gln 1145 1150 1155	3630
CAA AGC CAA CAT GGT GGA AGT CAT CCT GCA CCC AGT CCT GTT CAG CAC Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val Gln His 1160 1165 1170	3678
CAT CAG CAC CAG GCC GCC CAG GCT CTC CAT CTG GCC AGT CCA CAG CAG His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro Gln Gln 1175 1180 1185	3726
CAG TCA GCC ATT TAC CAC GCG GGG CTT GCG CCA ACT CCA CCC TCC ATG Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro Ser Met 1190 1195 1200	3774
ACA CCT GCC TCC AAC ACG CAG TCG CCA CAG AAT AGT TTC CCA GCA GCA Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser Phe Pro Ala Ala 1205 1210 1215 1220	3822
CAA CAG ACT GTC TTT ACG ATC CAT CCT TCT CAC GTT CAG CCG GCG TAT Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro Ala Tyr 1225 1230 1235	3870
ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA CAG TCA Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val Gln Ser 1240 1245 1250	3918
GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG CTA ATG Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met Leu Met 1255 1260 1265	3966
ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA AGT GCA Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln Ser Ala 1270 1275 1280	4014
CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT ATG ACG Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met Thr 1285 1290 1295 1300	4062
CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAA GGCTGCCCTG His Pro Ser Val Gln Ala His His Gln Gln Gln Leu * 1305 1310	4111
GAGGAACCGA AAGGCCAAAT TCCCTCCTCC CTTCTACTGC TTCTACCAAC TGGAAGCACA	4171
GAAAAGTAGA ATTCATTTA TTTTGTTTT AAAATATATA TGTTGATTTC TTGTAACATC	4231
CAATAGGAAT GCTAACAGTT CACTTGCAGT GGAAGATACT TGGACCGAGT AGAGGCATT	4291
AGGAACCTGG GGGCTATTCC ATAATTCCAT ATGCTGTTTC AGAGTCCCAG AGGTACCCCA	4351
GCTCTGCTTG CCGAAACTGG AAGTTATTTA TTTTTAATA ACCCTTGAAA GTCATGAACA	4411

CATCAGCTAG CAAAAGAAGT AACAAAGAGTG ATTCTTGCTG CTATTACTGC TAAAAAAA	4471
AAAAAAAAAA	4481

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1312 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Ser Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu
1 5 10 15

Ser Arg Arg Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln
20 25 30

Arg Pro Ala Arg Arg Ser Gly Arg Gly Gly Gly Ala Ala Pro Gly
35 40 45

Pro Tyr Pro Ser Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro
50 55 60

Ser Arg Gln Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn
65 70 75 80

Gly Asn Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly
85 90 95

Leu Gly Gly Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala
100 105 110

Ser Pro Gly Ala Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly
115 120 125

Ala Arg Ala Ser Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala
130 135 140

Pro Gly Cys Pro Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr
145 150 155 160

Met Ser Leu Lys Pro Gln
165 170 175

Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala
180 185 190

Ala Asn Val Arg Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala
195 200 205

Ala Ala Pro Ser Pro Ser Ser Ser Val Ser Ser Ser Ala Thr
210 215 220

Ala Pro Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly
225 230 235 240

Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile
245 250 255

Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr
260 265 270

Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile
275 280 285

Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu
290 295 300

Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg
305 310 315 320

Glu Glu Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val
325 330 335

Val Gln Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe
340 345 350

Thr Asp Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys
355 360 365

Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu
370 375 380

Glu Ala Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met
385 390 395 400

Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser
405 410 415

Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu
420 425 430

Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu
435 440 445

Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg
450 455 460

Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg
465 470 475 480

Glu Gly His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly
485 490 495

Gln Arg Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser
500 505 510

Pro Arg Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr
515 520 525

Ser His Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val
530 535 540

Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser
545 550 555 560

Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg
565 570 575

Ala Ala Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser
580 585 590

Arg Pro Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser
595 600 605

Thr Met Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro
610 615 620

Lys Ala Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly
625 630 635 640

Ser Ile Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu
645 650 655

Ala Ala Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp
660 665 670

Ser Ser Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg
675 680 685

Pro Arg Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro
690 695 700

Val Leu Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala
705 710 715 720

Met Pro Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn
725 730 735

Arg Ala Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp
740 745 750

Gln Arg Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn
755 760 765

Glu Thr Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro
770 775 780

Val Val Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys
785 790 795 800

Asn Asp Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln
805 810 815

Leu Leu Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys
820 825 830

Ala
Chom

Asp Lys Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser
835 840 845

Ser Asn Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser
850 855 860

Pro Ser Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr
865 870 875 880

Ser Gln Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp
885 890 895

Asp Lys Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr
900 905 910

Leu Asn Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro
915 920 925

Lys Pro Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser
930 935 940

Pro Ser Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro
945 950 955 960

Val Cys Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly
965 970 975

Val Gln Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln
980 985 990

Ala Lys Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp
995 1000 1005

Gln His His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro
1010 1015 1020

Pro Ile Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr
1025 1030 1035 1040

Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His
1045 1050 1055

Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn
1060 1065 1070

Ala Arg Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser
1075 1080 1085

Ser Ser Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr
1090 1095 1100

Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr
1105 1110 1115 1120

Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn
1125 1130 1135

Ala Thr Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro
 1140 1145 1150
 Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser
 1155 1160 1165
 Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala
 1170 1175 1180
 Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr
 1185 1190 1195 1200
 Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser
 1205 1210 1215
 Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val
 1220 1225 1230
 Gln Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala
 1235 1240 1245
 His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro
 1250 1255 1260
 Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu
 1265 1270 1275 1280
 Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe
 1285 1290 1295
 Pro Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3798 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
 - ii) MOLECULE TYPE: cDNA
 - ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 50..3457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCACGAGGT CCCCGCCCGG CGTGCGAGCC GGTGTATGGG CCGCTCACC ATG TCG
Met Ser
1

55

CTG AAG CCG CAG CCG CAG CCG CCC GCG CCC GCC ACT GGC CGC AAG CCC		103
Leu Lys Pro Gln Pro Gln Pro Pro Ala Pro Ala Thr Gly Arg Lys Pro		
5 10 15		
GGC GGC GGC CTG CTC TCG TCG CCC GGC GCC GCG CCG GCC TCG GCC GCG		151
Gly Gly Leu Leu Ser Ser Pro Gly Ala Ala Pro Ala Ser Ala Ala		
20 25 30		
GTG ACC TCG GCT TCC GTG GTG CCG GCC CCG GCG CCG GTG GCG TCT		199
Val Thr Ser Ala Ser Val Val Pro Ala Pro Ala Ala Pro Val Ala Ser		
35 40 45 50		
TCC TCG GCG GCC GCG GGC GGC GGG CGT CCC GGC CTG GGC AGA GGT CGG		247
Ser Ser Ala Ala Ala Gly Gly Arg Pro Gly Leu Gly Arg Gly Arg		
55 60 65		
AAC AGT AGC AAA GGA CTG CCT CAG CCT ACG ATT TCT TTT GAT GGA ATC		295
Asn Ser Ser Lys Gly Leu Pro Gln Pro Thr Ile Ser Phe Asp Gly Ile		
70 75 80		
TAT GCA AAC GTG AGG ATG GTT CAT ATA CTT ACG TCA GTT GTT GGA TCG		343
Tyr Ala Asn Val Arg Met Val His Ile Leu Thr Ser Val Val Gly Ser		
85 90 95		
AAA TGT GAA GTA CAA GTG AAA AAC GGA GGC ATA TAT GAA GGA GTT TTT		391
Lys Cys Glu Val Gln Val Lys Asn Gly Ile Tyr Glu Gly Val Phe		
100 105 110		
AAA ACA TAC AGT CCT AAG TGT GAC TTG GTA CTT GAT GCT GCA CAT GAG		439
Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His Glu		
115 120 125 130		
AAA AGT ACA GAA TCC AGT TCG GGG CCA AAA CGT GAA GAA ATA ATG GAG		487
Lys Ser Thr Glu Ser Ser Gly Pro Lys Arg Glu Glu Ile Met Glu		
135 140 145		
AGT GTT TTG TTC AAA TGC TCA GAC TTC GTT GTG GTA CAG TTT AAA GAT		535
Ser Val Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys Asp		
150 155 160		
ACA GAC TCC AGT TAT GCA CGG AGA GAT GCT TTT ACT GAC TCT GCT CTC		583
Thr Asp Ser Ser Tyr Ala Arg Arg Asp Ala Phe Thr Asp Ser Ala Leu		
165 170 175		
AGC GCA AAG GTG AAT GGT GAG CAC AAG GAG AAG GAC CTG GAG CCC TGG		631
Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro Trp		
180 185 190		
GAT GCA GGG GAG CTC ACG GCC AGC GAG GAG CTG GAG CTG GAG AAT GAT		679
Asp Ala Gly Glu Leu Thr Ala Ser Glu Glu Leu Glu Leu Glu Asn Asp		
195 200 205 210		
GTG TCT AAT GGA TGG GAC CCC AAT GAC ATG TTT CGA TAT AAT GAA GAG		727
Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn Glu Glu		
215 220 225		

AAT TAT GGT GTG GTG TCC ACA TAT GAT AGC AGT TTA TCT TCA TAT ACG Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser Tyr Thr 230 235 240	775
GTT CCT TTA GAA AGG GAC AAC TCA GAA GAA TTT CTT AAA CGG GAG GCA Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg Glu Ala 245 250 255	823
AGG GCA AAC CAG TTA GCA GAA GAA ATT GAA TCC AGT GCT CAG TAC AAA Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln Tyr Lys 260 265 270	871
GCT CGT GTC GCC CTT GAG AAT GAT GAC CGG AGT GAG GAA GAA AAA TAC Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu Lys Tyr 275 280 285 290	919
ACA GCA GTC CAG AGA AAC TGC AGT GAC CGG GAG GGG CAT GGC CCC AAC Thr Ala Val Gln Arg Asn Cys Ser Asp Arg Glu Gly His Gly Pro Asn 295 300 305	967
ACT AGG GAC AAT AAA TAT ATT CCT CCT GGA CAA AGA AAC AGA GAA GTC Thr Arg Asp Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg Glu Val 310 315 320	1015
CTA TCC TGG GGA AGT GGG AGA CAG AGC TCA CCA CGG ATG GGC CAG CCT Leu Ser Trp Gly Ser Gly Arg Gln Ser Ser Pro Arg Met Gly Gln Pro 325 330 335	1063
GGG CCA GGC TCC ATG CCG TCA AGA GCT GCT TCT CAC ACT TCA GAT TTC Gly Pro Gly Ser Met Pro Ser Arg Ala Ala Ser His Thr Ser Asp Phe 340 345 350	1111
AAC CCG AAC GCT GGC TCA GAC CAA AGA GTA GTT AAT GGA GGT GTT CCC Asn Pro Asn Ala Gly Ser Asp Gln Arg Val Val Asn Gly Gly Val Pro 355 360 365 370	1159
TGG CCA TCG CCT TGC CCA TCT CAT TCC TCT CGC CCA CCT TCT CGC TAC Trp Pro Ser Pro Cys Pro Ser His Ser Ser Arg Pro Pro Ser Arg Tyr 375 380 385	1207
CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CAT ACA CGG Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr His Thr Arg 390 395 400	1255
CCG CCC TCC AGG CCC CCC TCG AGG CCA TCC AGA CCC CCG TCT CAC CCC Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser His Pro 405 410 415	1303
TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA CGC ATG Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys Arg Met 420 425 430	1351
TCT TCA GAA GGA CCC CCA AGG ATG TCT CCA AAG GCA CAG CGC CAC CCT Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg His Pro 435 440 445 450	1399

CGG AAT CAC AGA GTC TCT GCT GGG AGA GGC TCC ATG TCT AGT GGC CTA Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Met Ser Ser Gly Leu 455 460 465	1447
GAA TTT GTA TCC CAC AAT CCC CCA AGT GAA GCA GCT GCT CCT CCA GTG Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Ala Pro Pro Val 470 475 480	1495
GCA AGG ACC AGT CCT GCA GGG GGA ACG TGG TCC TCA GTG GTC AGT GGG Ala Arg Thr Ser Pro Ala Gly Gly Thr Trp Ser Ser Val Val Ser Gly 485 490 495	1543
GTT CCA AGG TTA TCT CCC AAA ACT CAC AGA CCC AGG TCT CCC AGG CAG Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro Arg Gln 500 505 510	1591
AGC AGC ATT GGA AAC TCT CCC AGC GGG CCT GTG CTT GCT TCT CCC CAA Ser Ser Ile Gly Asn Ser Pro Ser Gly Pro Val Leu Ala Ser Pro Gln 515 520 525 530	1639
GCT GGC ATC ATC CCT GCA GAA GCC GTT TCC ATG CCT GTT CCC GCC GCA Ala Gly Ile Ile Pro Ala Glu Ala Val Ser Met Pro Val Pro Ala Ala 535 540 545	1687
TCT CCG ACT CCT GCC AGC CCT GCA TCC AAC AGA GCA CTG ACC CCA TCT Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Leu Thr Pro Ser 550 555 560	1735
ATT GAG GCA AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC TCT CCT Ile Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn Ser Pro 565 570 575	1783
GCA GGG AGT AAA GAA AAT GTT AAA GCA AGT GAA ACA TCA CCT AGC TTT Ala Gly Ser Lys Glu Asn Val Lys Ala Ser Glu Thr Ser Pro Ser Phe 580 585 590	1831
TCA AAA GCT GAC AAC AAA GGT ATG TCA CCA GTT GTT TCT GAA CAC AGA Ser Lys Ala Asp Asn Lys Gly Met Ser Pro Val Val Ser Glu His Arg 595 600 605 610	1879
AAA CAG ATT GAT GAC TTA AAG AAG TTT AAG AAT GAT TTT AGG TTA CAG Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg Leu Gln 615 620 625	1927
CCA AGC TCT ACA TCT GAA TCT ATG GAT CAA CTA CTA AGC AAA AAT AGA Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Ser Lys Asn Arg 630 635 640	1975
GAA GGA GAA AAG TCA CGA GAT TTG ATT AAA GAT AAA ACG GAA GCA AGT Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Thr Glu Ala Ser 645 650 655	2023
GCT AAG GAT AGT TTC ATT GAC AGC AGC AGC AGC AGC AAC TGT ACC Ala Lys Asp Ser Phe Ile Asp Ser Ser Ser Ser Ser Asn Cys Thr 660 665 670	2071

AGT GGC AGC AGC AAG ACC AAC AGC CCT AGC ATC TCC CCT TCC ATG CTT Ser Gly Ser Ser Lys Thr Asn Ser Pro Ser Ile Ser Pro Ser Met Leu 675 680 685 690	2119
AGT AAT GCA GAG CAC AAG AGG GGG CCT GAG GTC ACA TCC CAA GGG GTG Ser Asn Ala Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val 695 700 705	2167
CAG ACT TCC AGC CCA GCC TGC AAA CAA GAG AAG GAT GAC AGA GAA GAG Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Arg Glu Glu 710 715 720	2215
AAG AAA GAC ACA ACA GAG CAG GTT AGG AAA TCG ACA TTG AAT CCC AAT Lys Lys Asp Thr Thr Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn 725 730 735	2263
GCA AAG GAG TTC AAC CCT CGT TCT TTC TCT CAG CCA AAG CCT TCT ACT Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr 740 745 750	2311
ACC CCA ACG TCA CCT CGG CCT CAA GCA CAA CCC AGC CCA TCT ATG GTG Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val 755 760 765 770	2359
GGT CAT CAG CAG CCA GCT CCA GTG TAC ACT CAG CCT GTG TGC TTC GCA Gly His Gln Gln Pro Ala Pro Val Tyr Thr Gln Pro Val Cys Phe Ala 775 780 785	2407
CCC AAT ATG ATG TAT CCC GTC CCA GTG AGC CCG GGC GTA CAA CCT TTA Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu 790 795 800	2455
TAC CCA ATA CCT ATG ACG CCC ATG CCT GTG AAC CAA GCC AAG ACA TAT Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr 805 810 815	2503
AGA GCA GGT AAA GTA CCA AAT ATG CCC CAA CAG CGA CAA GAC CAA CAT Arg Ala Gly Lys Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His 820 825 830	2551
CAT CAA AGC ACC ATG ATG CAC CCA GCC TCC GCG GCA GGG CCA CCC ATC His Gln Ser Thr Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile 835 840 845 850	2599
GTA GCC ACC CCG CCC GCT TAC TCC ACT CAG TAC GTT GCC TAC AGC CCT Val Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro 855 860 865	2647
CAG CAG TTT CCC AAT CAG CCT TTG GTC CAG CAT GTG CCG CAT TAT CAG Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln 870 875 880	2695
TCT CAG CAT CCT CAT GTG TAC AGT CCT GTC ATA CAA GGT AAT GCC AGG Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg 885 890 895	2743

ATG ATG GCA CCA CCA GCA CAT GCT CAG CCT GGT TTA GTG TCT TCT TCA Met Met Ala Pro Pro Ala His Ala Gln Pro Gly Leu Val Ser Ser Ser 900 905 910	2791
GCT GCT CAG TTC GGG GCT CAC GAG CAG ACG CAC GCC ATG TAT GCA TGT Ala Ala Gln Phe Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys 915 920 925 930	2839
CCC AAA TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala 935 940 945	2887
ATT TCC ACC GGC TCC CTC GCT CAG CAG TAT GCA CAT CCT AAT GCC GCC Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Ala 950 955 960	2935
CTG CAT CCA CAT ACT CCC CAT CCT CAG CCT TCG GCC ACT CCC ACC GGA Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly 965 970 975	2983
CAG CAG CAA AGC CAG CAT GGT GGA AGT CAC CCT GCA CCC AGT CCT GTT Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val 980 985 990	3031
CAG CAC CAT CAG CAC CAG GCT GCC CAG GCT CTT CAT CTG GCC AGT CCA Gln His His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro 995 1000 1005 1010	3079
CAG CAG CAG TCG GCC ATT TAT CAT GCG GGG CTG GCA CCA ACA CCA CCT Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro 1015 1020 1025	3127
TCC ATG ACA CCT GCC TCT AAT ACA CAG TCT CCA CAG AGC AGT TTC CCA Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Ser Ser Phe Pro 1030 1035 1040	3175
GCA GCA CAA CAG ACA GTC TTC ACC ATC CAC CCT TCT CAT GTT CAG CCG Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro 1045 1050 1055	3223
GCA TAC ACC ACC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA Ala Tyr Thr Thr Pro Pro His Met Ala His Val Pro Gln Ala His Val 1060 1065 1070	3271
CAG TCA GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met 1075 1080 1085 1090	3319
CTA ATG ACG ACA CAG CCA CCC GGT CCC AAG GCC GCC CTC GCT CAA AGT Leu Met Thr Thr Gln Pro Pro Gly Pro Lys Ala Ala Leu Ala Gln Ser 1095 1100 1105	3367
GCA CTA CAG CCC ATT CCA GTT TCG ACA ACA GCG CAT TTC CCT TAT ATG Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met 1110 1115 1120	3415

A1
 Agmt.

ACG CAC CCT TCA CAA GCC CAC CAC CAA CAG CAG TTG TAA	3457
Thr His Pro Ser Val Gln Ala His His Gln Gln Leu	
1125 1130 1135	
GGCTGCCTTG GAGGAACCGA AAGGCCAAAT CCCTCTTCC CTTCTCTGCT TCTGCCAAC	3517
GGAAGCACAG AAAACTAGAA CTTCATTGAT TTTGTTTTT AAAAGATACA CTGATTAAAC	3577
ATCTGATAGG AATGCTAACCA GCTCACTTGC AGTGGAGGAT GTTTTGGACC GAGTAGAGGC	3637
ATGTAGGGAC TTGTGGCTGT TCCATAATT CATGTGCTGT TGCAAGGTCC TGCAAGTACC	3697
CAGCTCTGCT TGCTGAAACT GGAAGTTATT TATTTTTAA TGGCCCTTGA GAGTCATGAA	3757
CACATCAGCT AGCAACAGAA GTAACAAGAG TGATTCTTGC T	3798

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1135 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Leu Lys Pro Gln Pro Gln Pro Pro Ala Pro Ala Thr Gly Arg	
1 5 10 15	
Lys Pro Gly Gly Gly Leu Leu Ser Ser Pro Gly Ala Ala Pro Ala Ser	
20 25 30	
Ala Ala Val Thr Ser Ala Ser Val Val Pro Ala Pro Ala Ala Pro Val	
35 40 45	
Ala Ser Ser Ser Ala Ala Ala Gly Gly Gly Arg Pro Gly Leu Gly Arg	
50 55 60	
Gly Arg Asn Ser Ser Lys Gly Leu Pro Gln Pro Thr Ile Ser Phe Asp	
65 70 75 80	
Gly Ile Tyr Ala Asn Val Arg Met Val His Ile Leu Thr Ser Val Val	
85 90 95	
Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly	
100 105 110	
Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala	
115 120 125	
His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile	
130 135 140	
Met Glu Ser Val Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe	
145 150 155 160	

Lys Asp Thr Asp Ser Ser Tyr Ala Arg Arg Asp Ala Phe Thr Asp Ser
165 170 175

Ala Leu Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu
180 185 190

Pro Trp Asp Ala Gly Glu Leu Thr Ala Ser Glu Glu Leu Glu Leu Glu
195 200 205

Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn
210 215 220

Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser
225 230 235 240

Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg
245 250 255

Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln
260 265 270

Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu
275 280 285

Lys Tyr Thr Ala Val Gln Arg Asn Cys Ser Asp Arg Glu Gly His Gly
290 295 300

Pro Asn Thr Arg Asp Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg
305 310 315 320

Glu Val Leu Ser Trp Gly Ser Gly Arg Gln Ser Ser Pro Arg Met Gly
325 330 335

Gln Pro Gly Pro Gly Ser Met Pro Ser Arg Ala Ala Ser His Thr Ser
340 345 350

Asp Phe Asn Pro Asn Ala Gly Ser Asp Gln Arg Val Val Asn Gly Gly
355 360 365

Val Pro Trp Pro Ser Pro Cys Pro Ser His Ser Ser Arg Pro Pro Ser
370 375 380

Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr His
385 390 395 400

Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser
405 410 415

His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys
420 425 430

Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg
435 440 445

His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Met Ser Ser
450 455 460

Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Ala Pro
465 470 475 480

Pro Val Ala Arg Thr Ser Pro Ala Gly Gly Thr Trp Ser Ser Val Val
485 490 495

Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro
500 505 510

Arg Gln Ser Ser Ile Gly Asn Ser Pro Ser Gly Pro Val Leu Ala Ser
515 520 525

Pro Gln Ala Gly Ile Ile Pro Ala Glu Ala Val Ser Met Pro Val Pro
530 535 540

Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Leu Thr
545 550 555 560

Pro Ser Ile Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn
565 570 575

Ser Pro Ala Gly Ser Lys Glu Asn Val Lys Ala Ser Glu Thr Ser Pro
580 585 590

Ser Phe Ser Lys Ala Asp Asn Lys Gly Met Ser Pro Val Val Ser Glu
595 600 605

His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg
610 615 620

Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Ser Lys
625 630 635 640

Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Thr Glu
645 650 655

Ala Ser Ala Lys Asp Ser Phe Ile Asp Ser Ser Ser Ser Ser Asn
660 665 670

Cys Thr Ser Gly Ser Ser Lys Thr Asn Ser Pro Ser Ile Ser Pro Ser
675 680 685

Met Leu Ser Asn Ala Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln
690 695 700

Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Arg
705 710 715 720

Glu Glu Lys Lys Asp Thr Thr Glu Gln Val Arg Lys Ser Thr Leu Asn
725 730 735

Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro
740 745 750

Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser
755 760 765

*All
done*

Met Val Gly His Gln Gln Pro Ala Pro Val Tyr Thr Gln Pro Val Cys
770 775 780

Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln
785 790 795 800

Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys
805 810 815

Thr Tyr Arg Ala Gly Lys Val Pro Asn Met Pro Gln Gln Arg Gln Asp
820 825 830

Gln His His Gln Ser Thr Met Met His Pro Ala Ser Ala Ala Gly Pro
835 840 845

Pro Ile Val Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr
850 855 860

Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His
865 870 875 880

Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn
885 890 895

Ala Arg Met Met Ala Pro Pro Ala His Ala Gln Pro Gly Leu Val Ser
900 905 910

Ser Ser Ala Ala Gln Phe Gly Ala His Glu Gln Thr His Ala Met Tyr
915 920 925

Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr
930 935 940

Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn
945 950 955 960

Ala Ala Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro
965 970 975

Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser
980 985 990

Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala
995 1000 1005

Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr
1010 1015 1020

Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Ser Ser
1025 1030 1035 1040

Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val
1045 1050 1055

Gln Pro Ala Tyr Thr Thr Pro Pro His Met Ala His Val Pro Gln Ala
1060 1065 1070

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro
1075 1080 1085

Met Met Leu Met Thr Thr Gln Pro Pro Gly Pro Lys Ala Ala Leu Ala
1090 1095 1100

Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro
1105 1110 1115 1120

Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
1125 1130 1135

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGCCCTCA CCATGTCG 18

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGGCTTGCG GACATTGG 18

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGCGGGCTGC CAATGTCC

18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTAACCGTTC GGCGCCCG

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCTCCCGGC GGCTCCTT

18

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCTGCTGCT GCTGGGGCTT CAG

23

(2) INFORMATION FOR SEQ ID NO:12:

*Q1
Cont.*

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGCCCCGCTC CTCACGTGT

19

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCCCCGGAGA AAGCAACC

18

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCGTTGCCGT TGCTACCA

18

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCTCATGTG CGGCATCAAG

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Tyr Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Gln Gln Gln Gln
1 5 10 15

Gln
20 25 30

Gln Pro Pro Pro Ala Ala Ala Asn Val Arg Lys Pro Gly Gly Ser Gly
35 40 45

Leu Leu Ala Ser Pro Ala Ala Pro Ser Pro Ser Ser Ser Ser Val
50 55 60

Ser Ser Ser Ser Ala Thr Ala Pro Ser Ser Val Val Ala Ala Thr Ser
65 70 75 80

Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly
85 90 95

Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg
100 105 110

Met Val His Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln
115 120 125

Val Lys Asn Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro
130 135 140

Lys Cys Asp Leu Val Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser
145 150 155 160

Ser Ser Gly Pro Lys Arg Glu Glu Ile Met Glu Ser Ile Leu Phe Lys
165 170 175

Cys Ser Asp Phe Val Val Val Gln Phe Lys Asp Met Asp Ser Ser Tyr
180 185 190

Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala Ile Ser Ala Lys Val Asn
 195 200 205
 Gly Glu His Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu
 210 215 220
 Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu Asn Asp Val Ser Asn Gly
 225 230 235 240
 Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val
 245 250 255
 Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu
 260 265 270
 Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln
 275 280 285
 Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala
 290 295 300
 Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln
 305 310 315 320
 Arg Asn Ser Ser Glu Arg Glu Gly His Ser Ile Asn Thr Arg Glu Asn
 325 330 335
 Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg
 340 345

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro Pro
 1 5 10 15
 Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser Pro
 20 25 30
 Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val Pro
 35 40 45
 Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Gly Gly Gly
 50 55 60

*AI
Cont.*

Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Ser Lys Gly Leu Pro Gln
65 70 75 80

Pro Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Val Arg Met Val His
85 90 95

Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn
100 105 110

Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp
115 120 125

Leu Val Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly
130 135 140

Pro Lys Arg Glu Glu Ile Met Glu Ser Val Leu Phe Lys Cys Ser Asp
145 150 155 160

Phe Val Val Val Gln Phe Lys Asp Thr Asp Ser Ser Tyr Ala Arg Arg
165 170 175

Asp Ala Phe Thr Asp Ser Ala Leu Ser Ala Lys Val Asn Gly Glu His
180 185 190

Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Ser
195 200 205

Glu Glu Leu Glu Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn
210 215 220

Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr
225 230 235 240

Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser
245 250 255

Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu
260 265 270

Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp
275 280 285

Asp Arg Ser Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Cys Ser
290 295 300

Asp Arg Glu Gly His Gly Pro Asn Thr Arg Asp Asn Lys Tyr Ile Pro
305 310 315 320

Pro Gly Gln Arg Asn Arg
325

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

A1
Cont

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Ala Pro Gln Pro Pro Pro Gln Gln His Gln Glu Arg Pro Gly
1 5 10 15

Ala Ala Ala Ile Gly Ser Ala Arg Gly Gln Ser Thr Gly Lys Gly Pro
20 25 30

Pro Gln Ser Pro Val Phe Glu Gly Val Tyr Asn Asn Ser Arg Met Leu
35 40 45

His Phe Leu Thr Ala Val Val Gly Ser Thr Cys Asp Val Lys Val Lys
50 55 60

Asn Gly Thr Thr Tyr Glu Gly Ile Phe Lys Thr Leu Ser Ser Lys Phe
65 70 75 80

Glu Leu Ala Val Asp Ala Val His Arg Lys Ala Ser Glu Pro Ala Gly
85 90 95

Gly Pro Arg Arg Glu Asp Ile Val Asp Thr Met Val Phe Lys Pro Ser
100 105 110

Asp Val Met Leu Val His Phe Arg Asn Val Asp Phe Asn Tyr Ala Thr
115 120 125

Lys Asp Lys Phe Thr Asp Ser Ala Ile Ala Met Asn Ser Lys Val Asn
130 135 140

Gly Glu His Lys Glu Lys Val Leu Gln Arg Trp Glu Gly Gly Asp Ser
145 150 155 160

Asn Ser Asp Asp Tyr Asp Leu Glu Ser Asp Met Ser Asn Gly Trp Asp
165 170 175

Pro Asn Glu Met Phe Lys Phe Asn Glu Glu Asn Tyr Gly Val Lys Thr
180 185 190

Thr Tyr Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Lys Asp
195 200 205

Asn Ser Glu Glu Phe Arg Gln Arg Glu Leu Arg Ala Ala Gln Leu Ala
210 215 220

Arg Glu Ile Glu Ser Ser Pro Gln Tyr Arg Leu Arg Ile Ala Met Glu
225 230 235 240

Asn Asp Asp Gly Arg Thr Glu Glu Lys His Ser Ala Val Gln Arg
245 250 255

Gln Gly Ser Gly Arg Glu Ser Pro Ser Leu Ala Ser Arg Glu Gly Lys
260 265 270

A1
Tyr Ile Pro
275
conclude
